

FIG. 1A

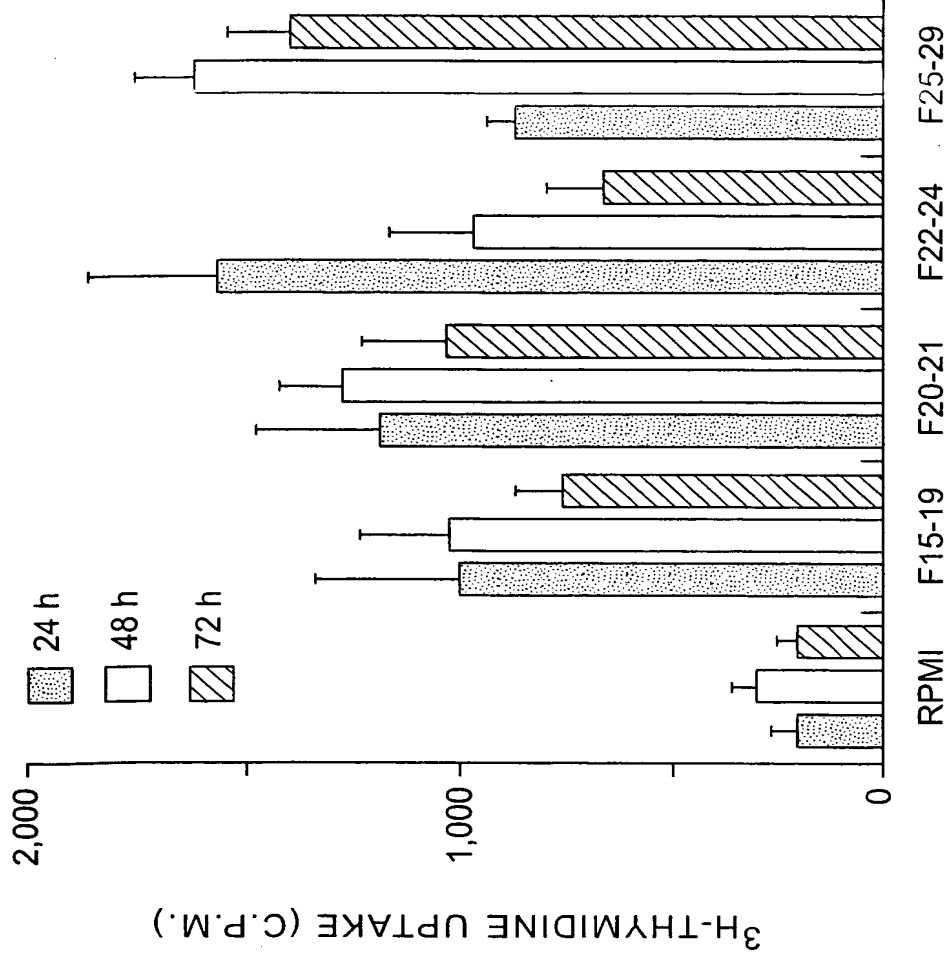


FIG. 1B

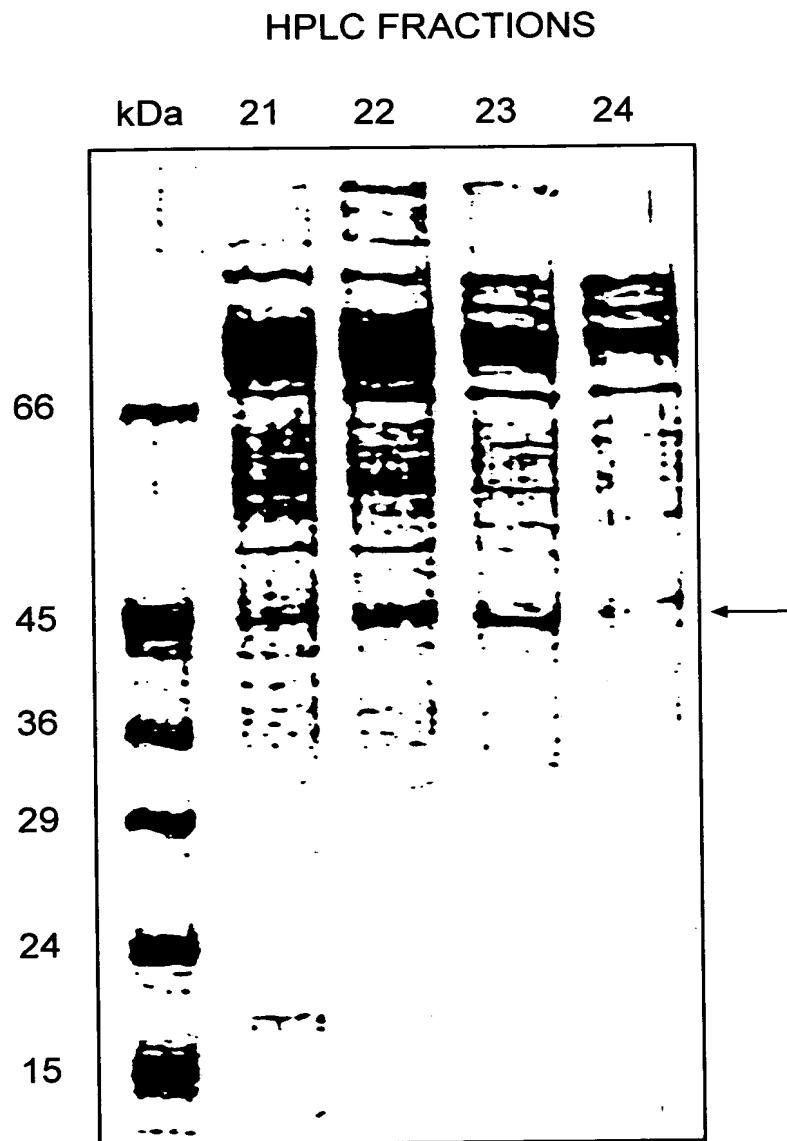


FIG. 1C

Tc	MRKSVCPKQKFFFSAPFFFFFCVFFLLISRTGQEKLLFDQKYKIIKGEKKEKKKNQRANRREHQKREIMREKKS	75
Cs	-----MKFSKG	6
Pa	-----MQR	3
TC	FTCIDMHTEGEAAARIVTSGLPHIPGSNMAEKAYLQENMDYLRRGIMLEPRGHDDMFGAFLDPIIEGADLGMVF	150
Cs	IHAIDSHTMGEPTRIIVGGIPQINGETMADKKKYLEDNLDYVRTALMHEPRGHNDMFGSIITSSNNKEADFGIIF	81
Pa	IRIIDSHTGGEPTRLVIGGFDPDLGQGDMAERRRLLGERHDAWRAACILEPRGSDVLVGALLCAPVDPEACAGVIF	78
TC	MDTGGYLNMCCHNSIAAVTAAVETGIVSVPAKATNVPVVDTPAGLVRGTAHLQSGTESEVSNASIIINVPSFLYQ	225
Cs	MDGGYLNMCCHGCSIGAA TVAVETGMVEMVEPTNIN--MEAPAGLIKAKVMVEN---EKVKEVSITNVPSFLYM	151
Pa	FNNSGYLGMCGHGTIGLVASLAHLGRIGPV-----HRIETPVGEVEATLH-----EDGSVSVRNVPAYRYR	140
TC	QDVVVVLPKPYGEVRVDIAFGGNFFAIVPAEQLGIDISVQNLSRLQEAAGELLRTEINRSVKVQHPQLPHINTVDC	300
Cs	EDAKLEVPSLNKTIITFDISFGGSFFAIIHAKELGVKVTESQVDVLKKGIEIRDLINEKIKVQHPLEHIKTVDL	226
Pa	RQVSVEVPGI-GRVSGDIAWGGNWFVLVAGH--GQRLAGDNLDAITAYTVAVQQALDD----QDIRGEDGGAIDH	208
TC	VEIYGPPPTNPEANYKNVVFNGNRQADR	371
Cs	VEIYDEPSNPEATYKNVVFNGQGVDR	297
Pa	IELFAD--DPHADSRNFVLCPCGKAYDR	279
	SPCGT	
	GTSAKMATLYAKGQLRIGETFVYESILGSLFQGRV--LGEE	
	SPCGT	
	GTSAKLATLYKKGHLKIDEFVYESITGTMFKGRV--LEET	
	SPCGT	
	GTSAKLAADCKLLPGQPWRQASVIGSQFEGRYEWLDGQ	
TC	RIPGVKVPVTKDAEEGMLVVTAETGKAFIMGFNTMLFDPTDPFKNGFTLKQ*	423
Cs	KVGEFD-----AIIPEITGGAYITGFNFHVIDPEDPLKYGFTV*--	335
Pa	PGGPVPTIRGRAHVSAEATLLADDDPFAWGIRR*-----	314

FIG. 2

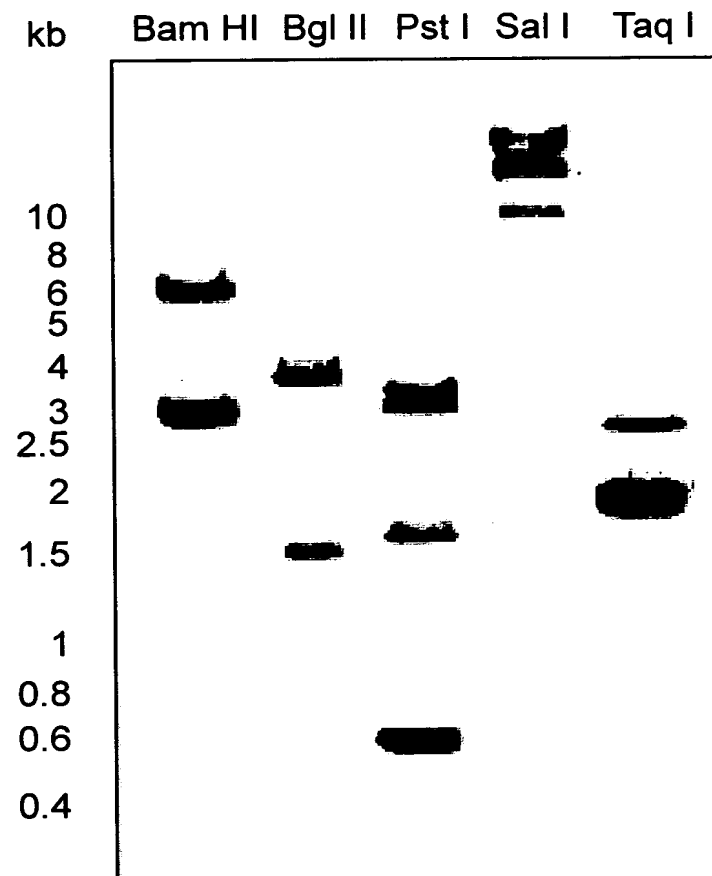


FIG. 3A

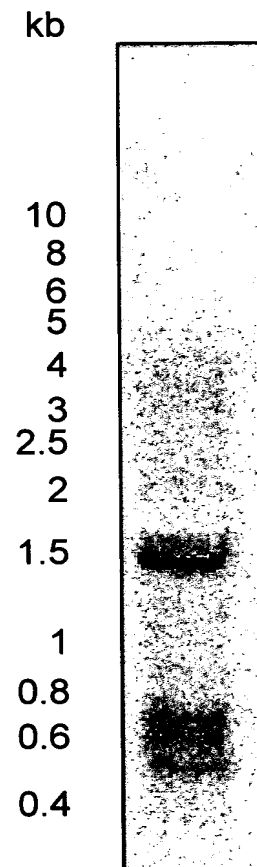


FIG. 3B

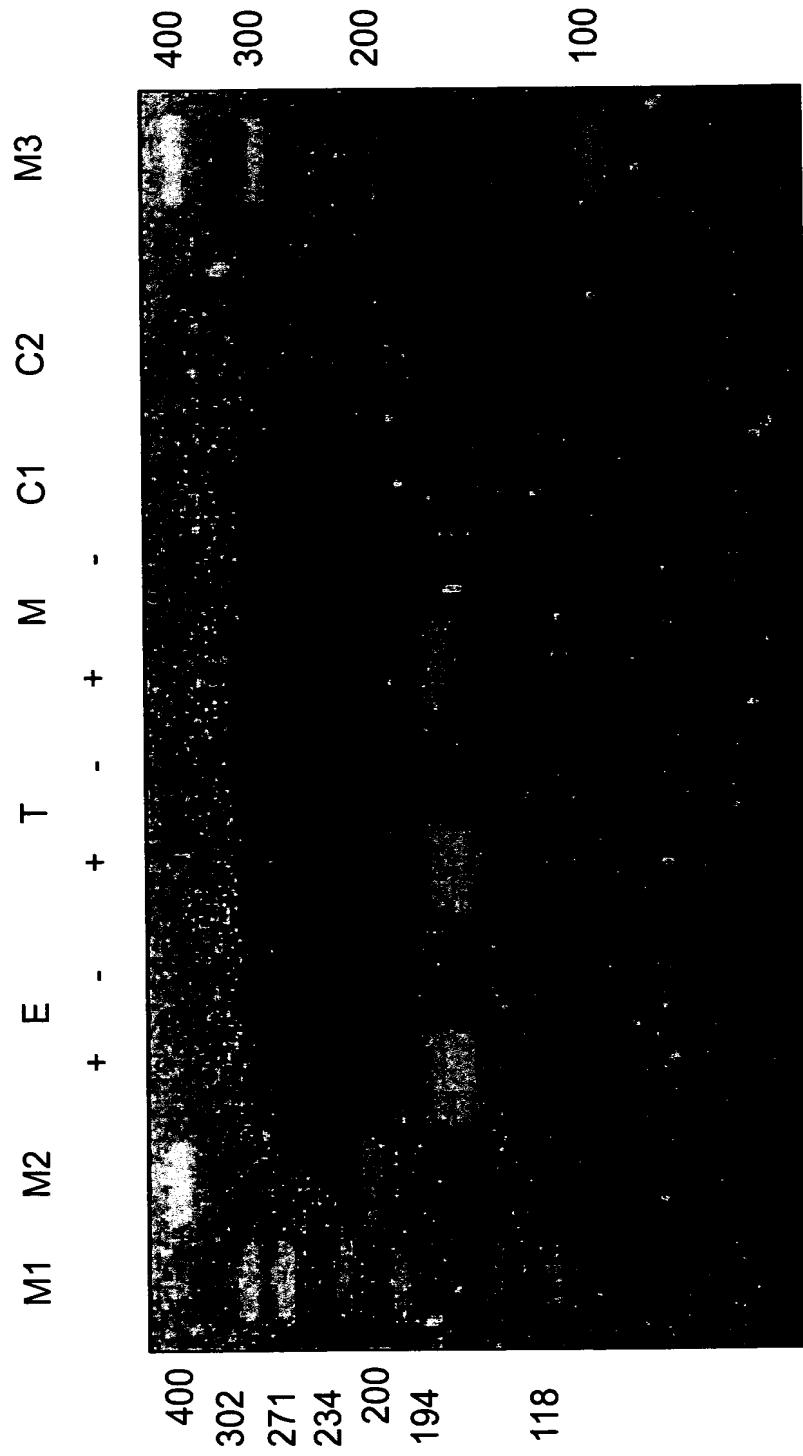


FIG. 3C

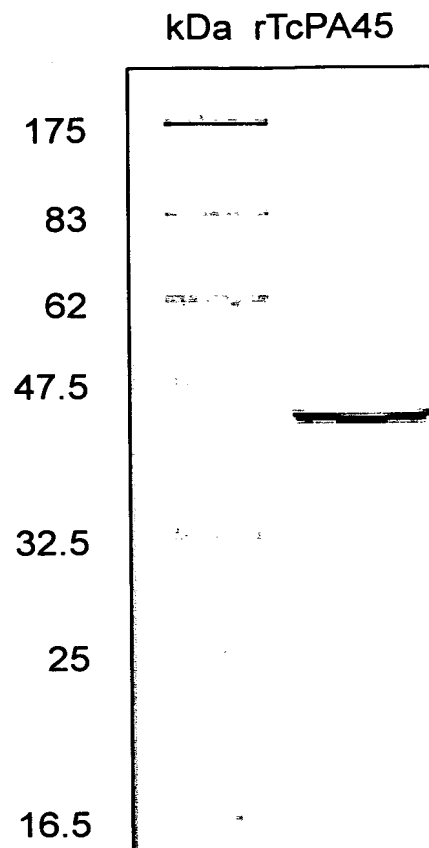


FIG. 4A

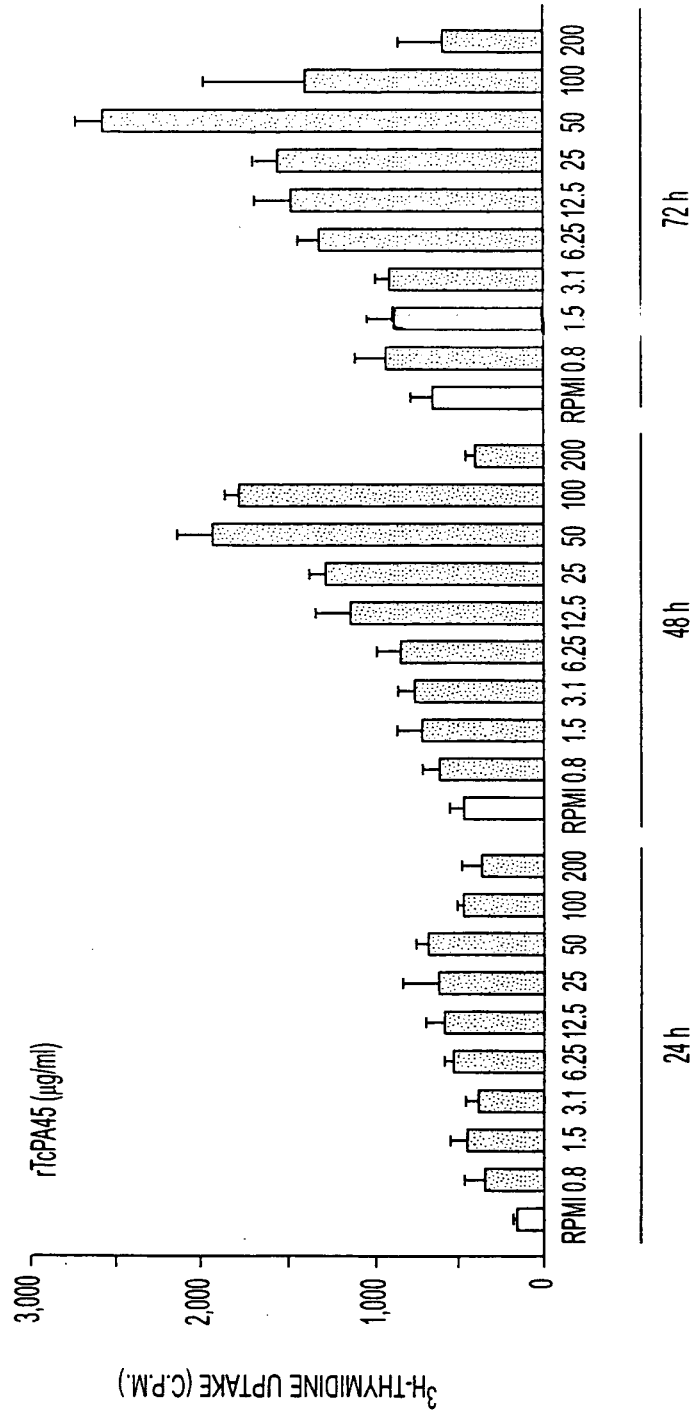


FIG. 4B

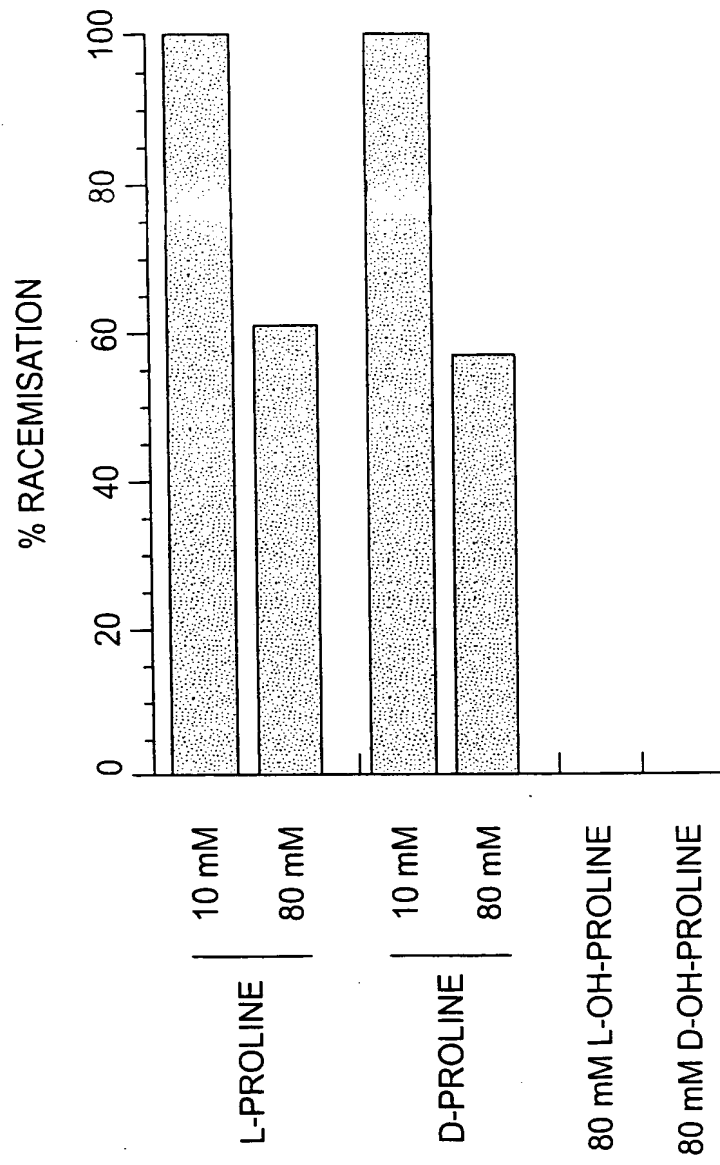


FIG. 4C

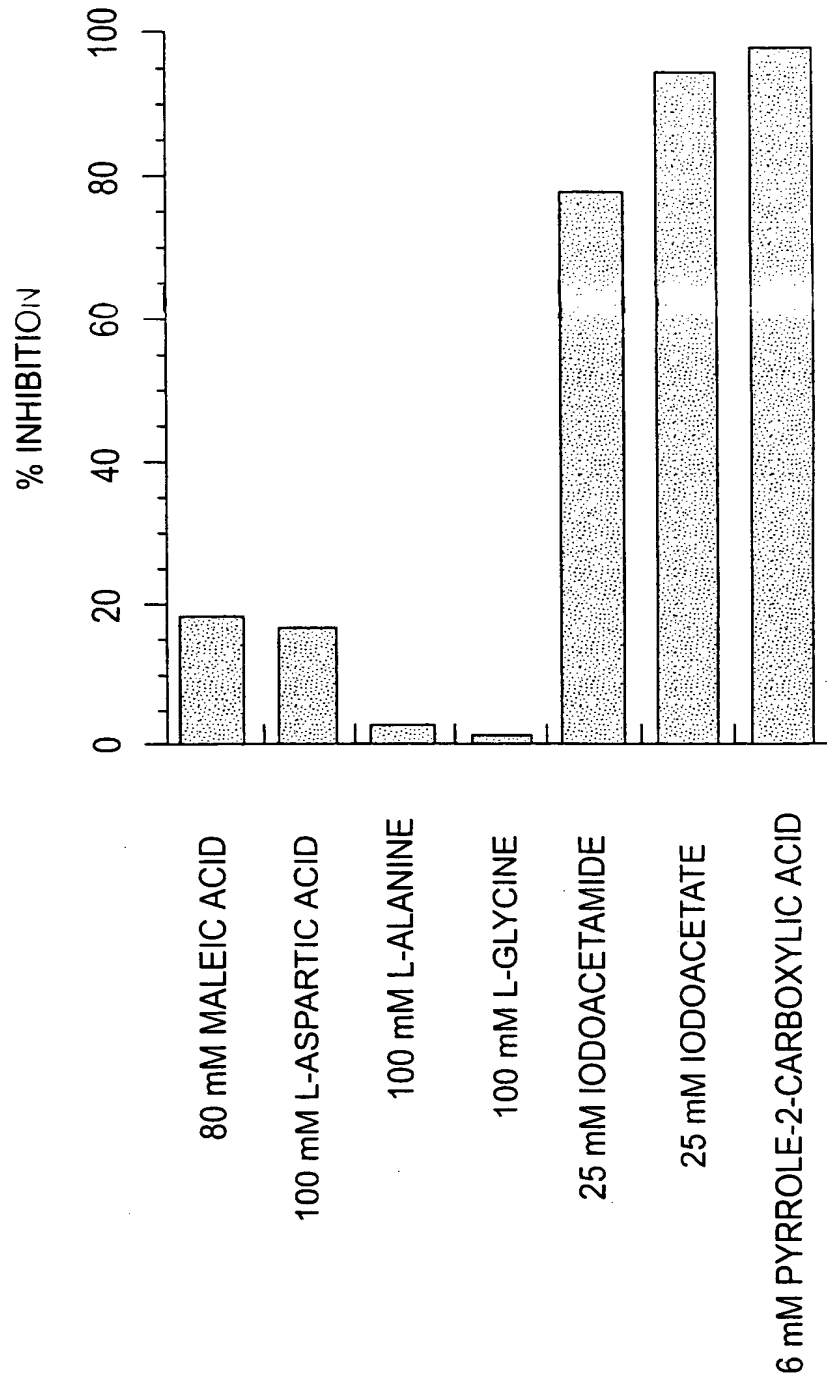


FIG. 4D

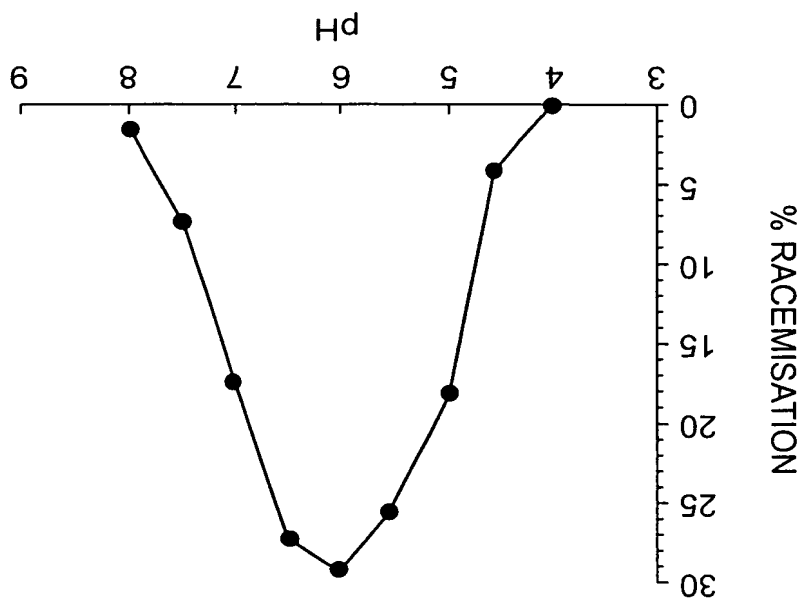


FIG. 4E

FIG. 5A

CGCAGTGTGAAGGTTACAGCACCCCTCAGCTGCCCCCATATTAACTGTGGACTGTGTGAGATATACGGTCCGCCAACGAACCCGGAGGCA 970
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A 312
AACTACAAGAACGTTGTGATATTGGCAATGCCAGGCGGATCGCTCTCCATGTGGACAGGCCAGCCCAAGATGGCAACACATTTAT 1060
N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L L Y 342
GCCAAGGCCAGCTTCGCATCGGAGAGACTTTTGTGTACGAGAGCATACTCGGCTCACTCTCCAGGCCAGGGTACTTGGGGAGGAGCCGA 1150
A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 372
ATACCGGGGTGAAGGTGCCGTGACCAAGATGCCAGGAAGGATGCTCGTTGTAACGGCAGAAATTACTGGAAGGCTTTTATCATG 1240
I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 402
GGTTTCAACACCATGCTGTTGACCCCAACGGATCCGTTTAAGAACGGATTACATTAAGCAGTAGATCTGGTAGAGCACAGAACTATT 1330
G F N T M L F D P T D P F K N G F T L K Q 423
GGGGAACACGTGCGAACAGGTGCTGTACGTGAAGGTATTGAATGAATCGTTTTTTTATTTTATTTTATTTTATTTATAGTGCATT 1420

ATTATTAAATTTTTTTTTTTGGGTTTCAACGGTACC CGTGGAGCAGGAAGCGATAGCGGCCGGACAATTTTTCGCTTTTAT 1510

TTTTCATTTTCATCTTCCTACCCAAACCCCTTGGTTCCACCGGTCCGGCGGGGTCTTGTGGGTGGAGGAGTCCTAAATCCCGCACCTCGG 1600

AGGAATAACATATTCAATTCATATCTTGAATCAAAGGCAT 1651

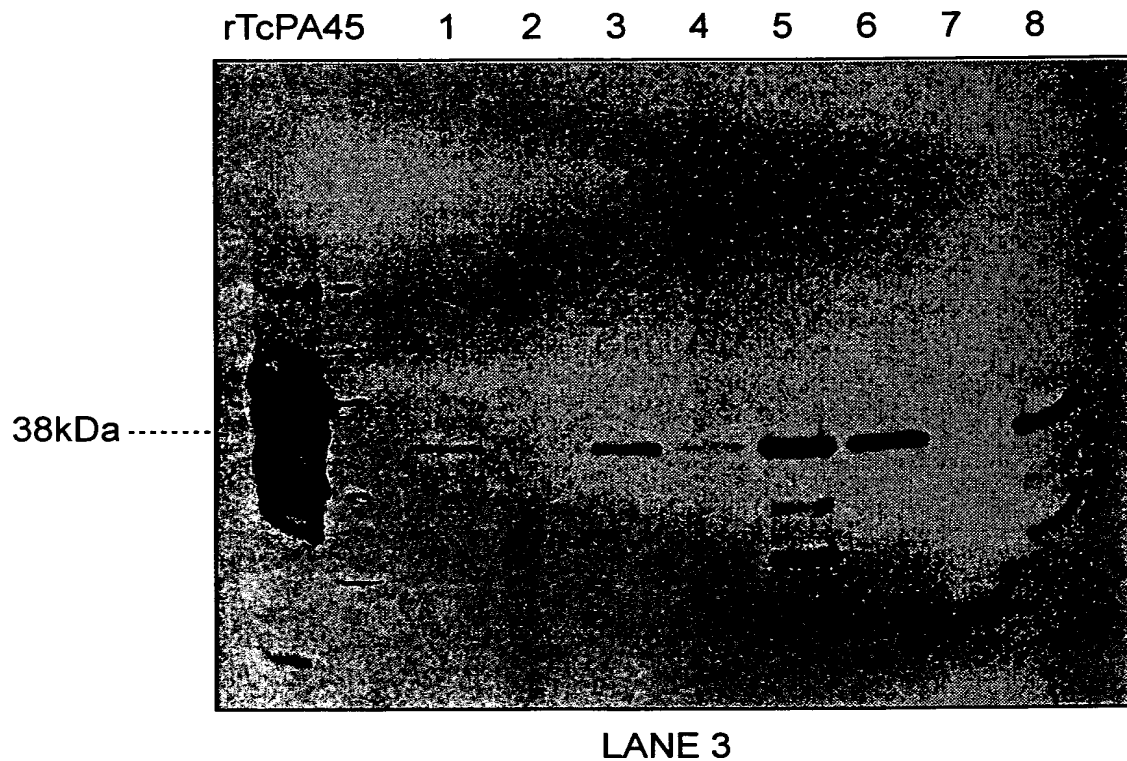
POLYADENILATION SITE

OBS: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS FOR CLONING

NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

FIG. 5B

WESTERN BLOT



SOLUBLE FRACTION OF EPIMASTIGOTES EXTRACT (CYTOSOLIC)
REVEALED WITH ANTIBODY DIRECTED TO rTcPA45

----- DEMONSTRATES THE EXISTANCE OF AN INTRACYTOPLASMIC
FORM OF TcPA45 IN THE PARASITE

FIG. 6

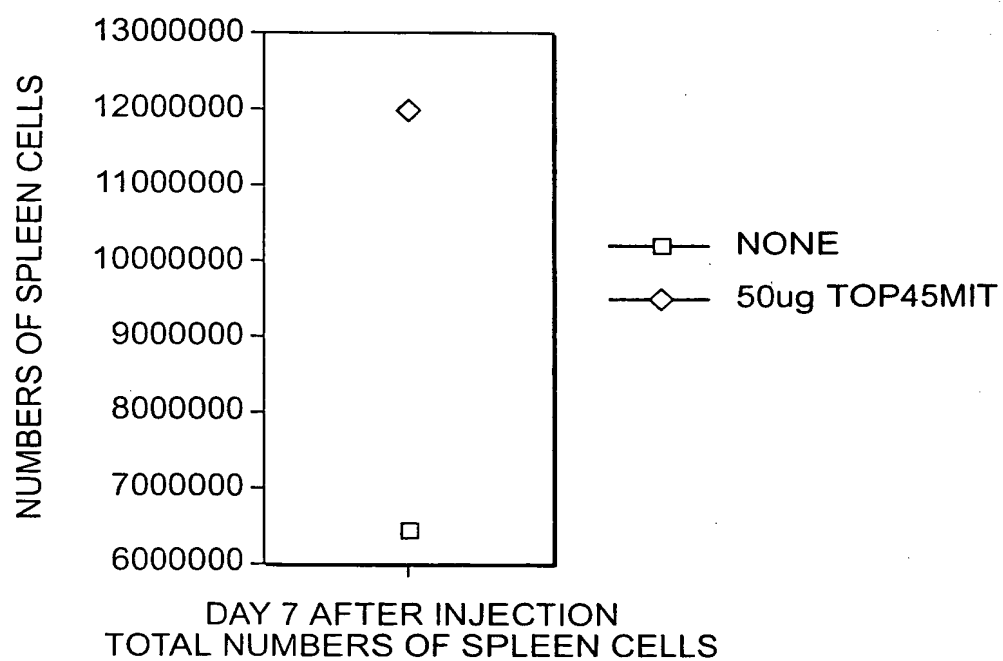
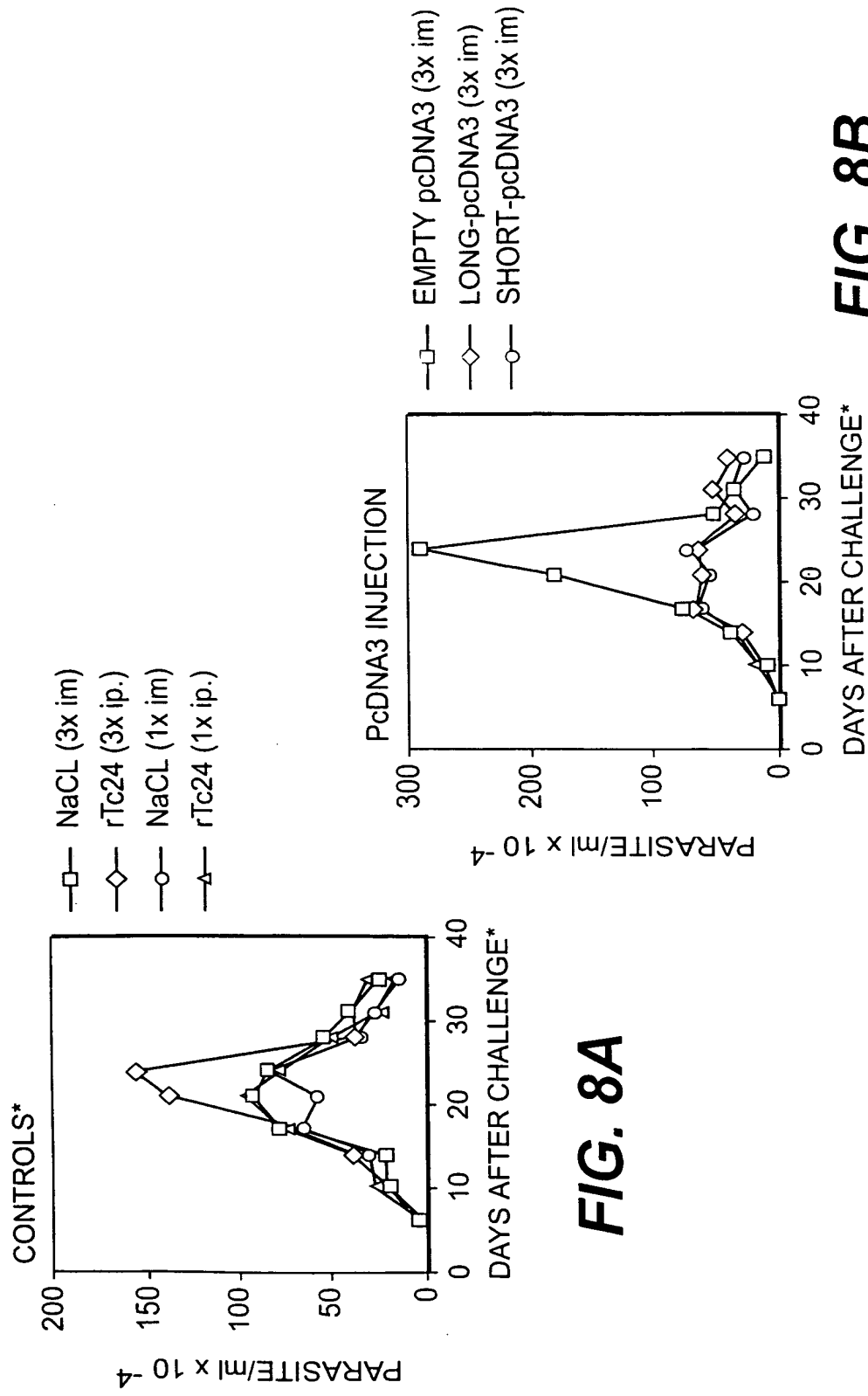


FIG. 7



- | | | |
|----------------------------|----------------------------|----------------------------|
| —□— EMPTY pcDNA3 (1x i.m.) | —□— EMPTY VR 1020 (3 i.m.) | —□— EMPTY VR 1020 (1 i.m.) |
| —◇— LONG pcDNA3 (1x i.m.) | —◇— LONG VR 1020 (3 i.m.) | —◇— LONG VR 1020 (1 i.m.) |
| —○— SHORT pcDNA3 (1x i.m.) | —○— SHORT VR 1020 (3 i.m.) | —○— SHORT VR 1020 (1 i.m.) |

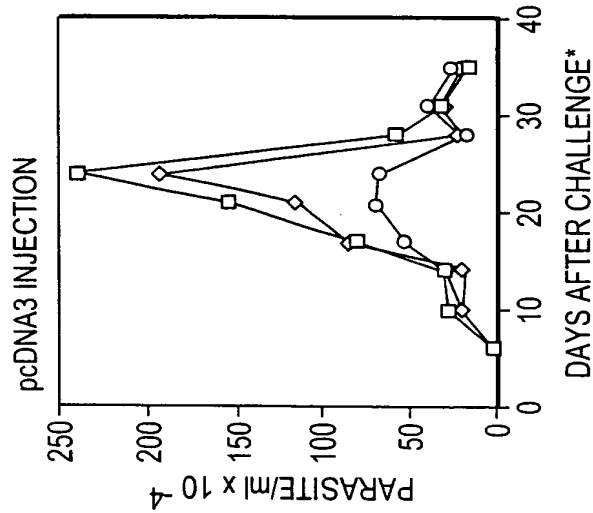


FIG. 8C

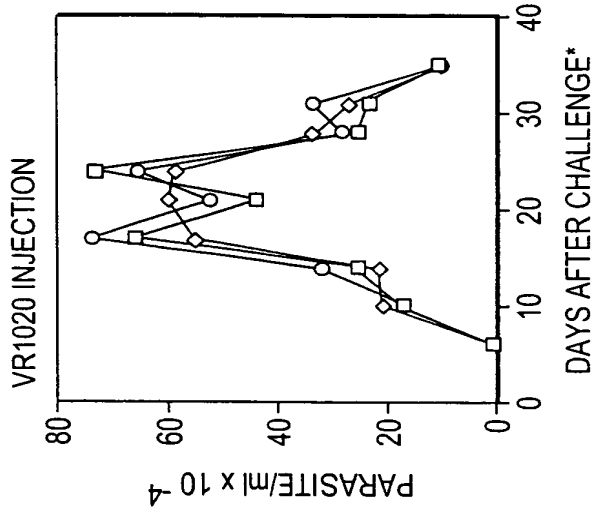


FIG. 8D

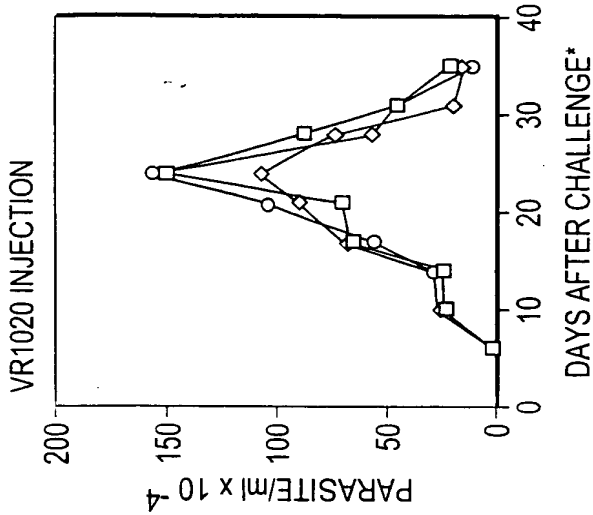


FIG. 8E

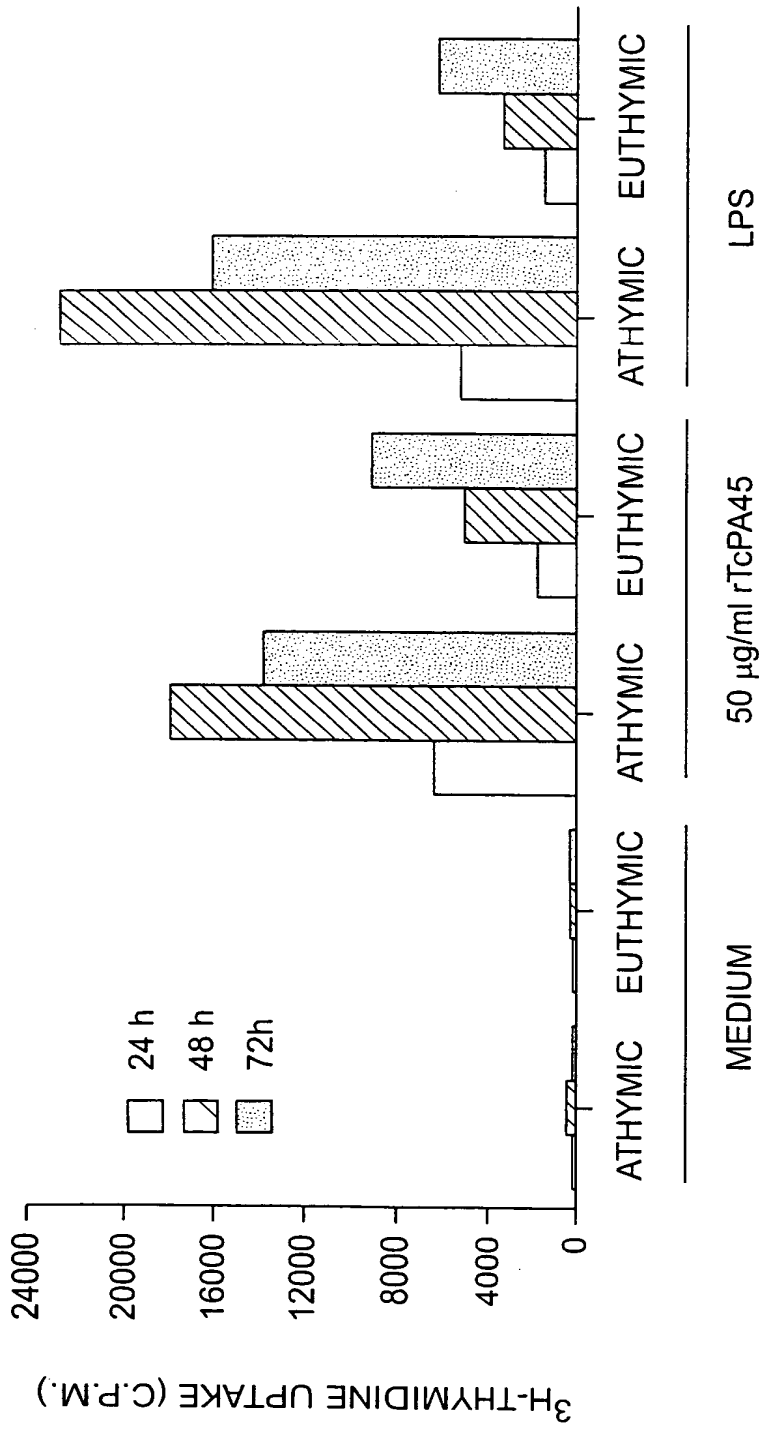


FIG. 9

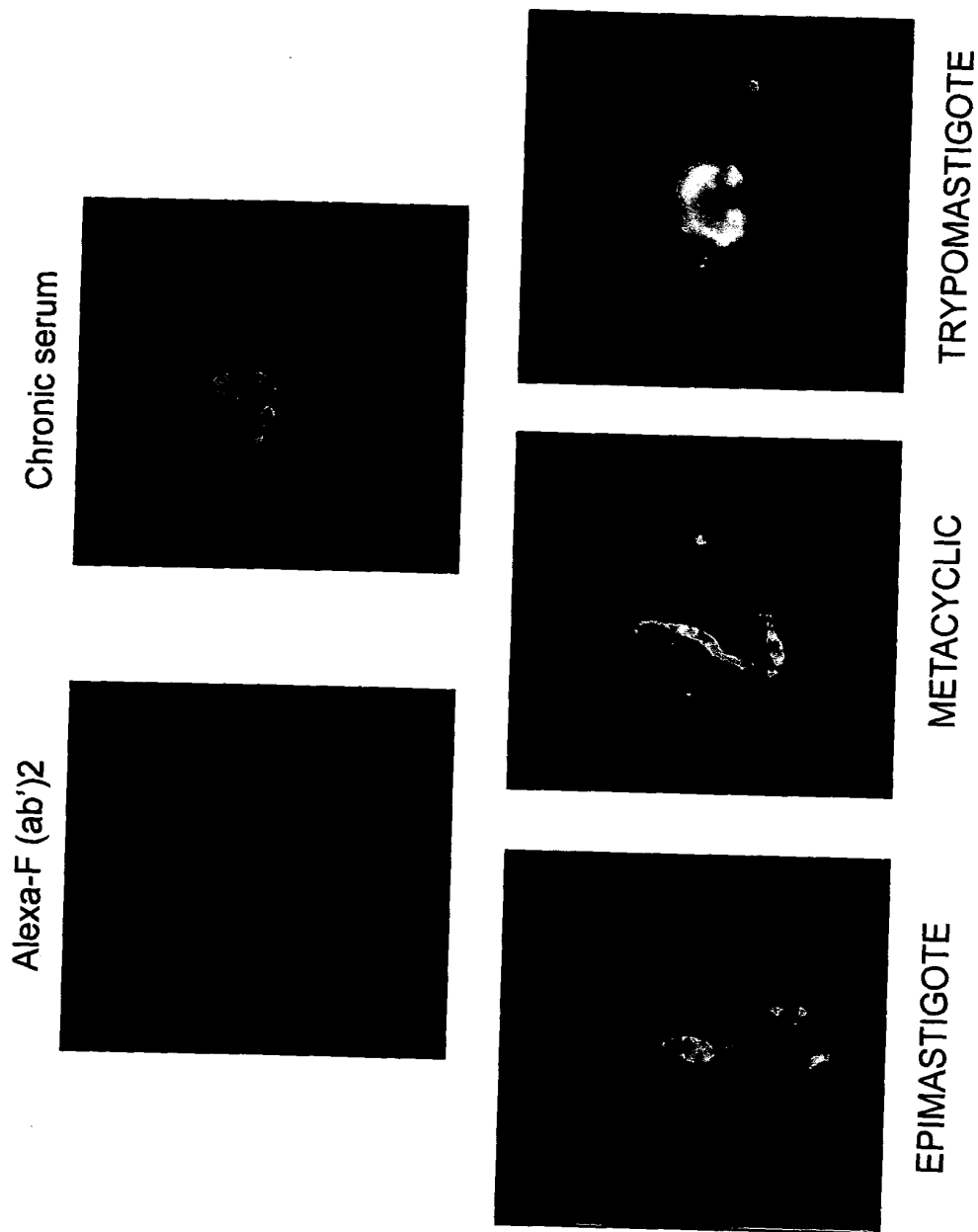


FIG. 10A

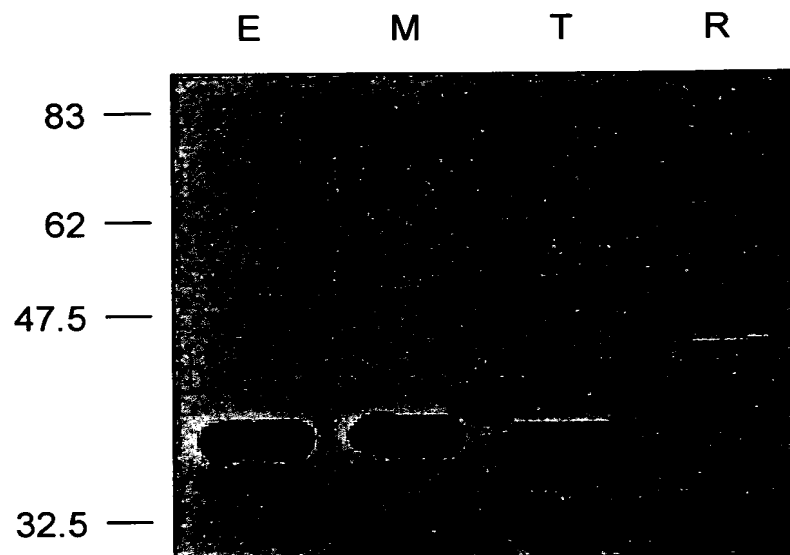


FIG. 10B

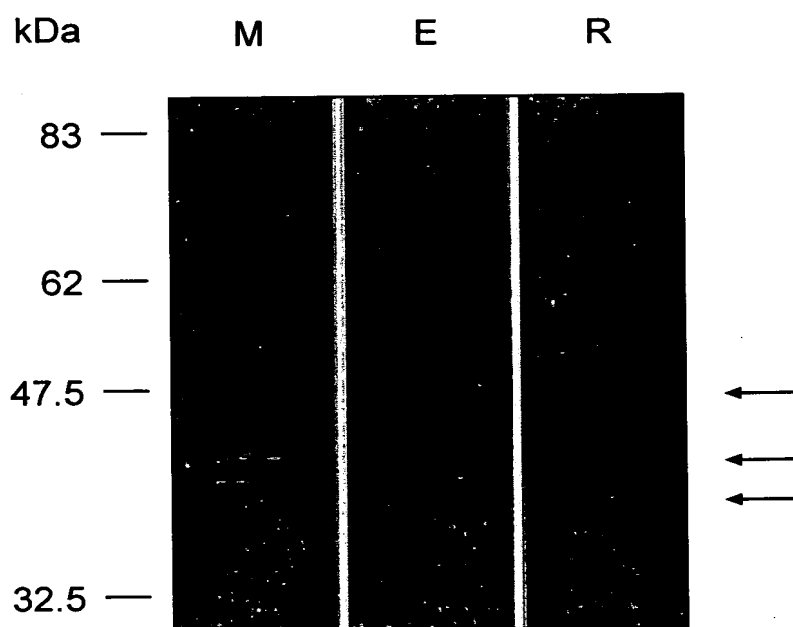


FIG. 10C

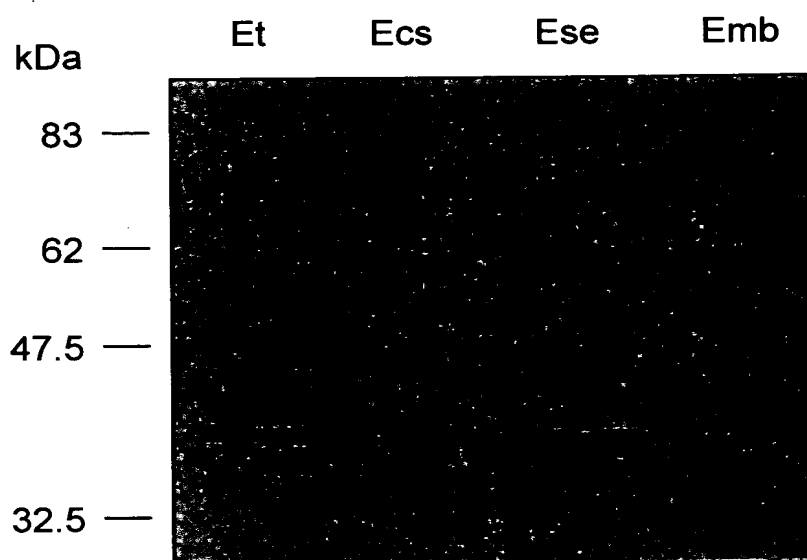


FIG. 10D

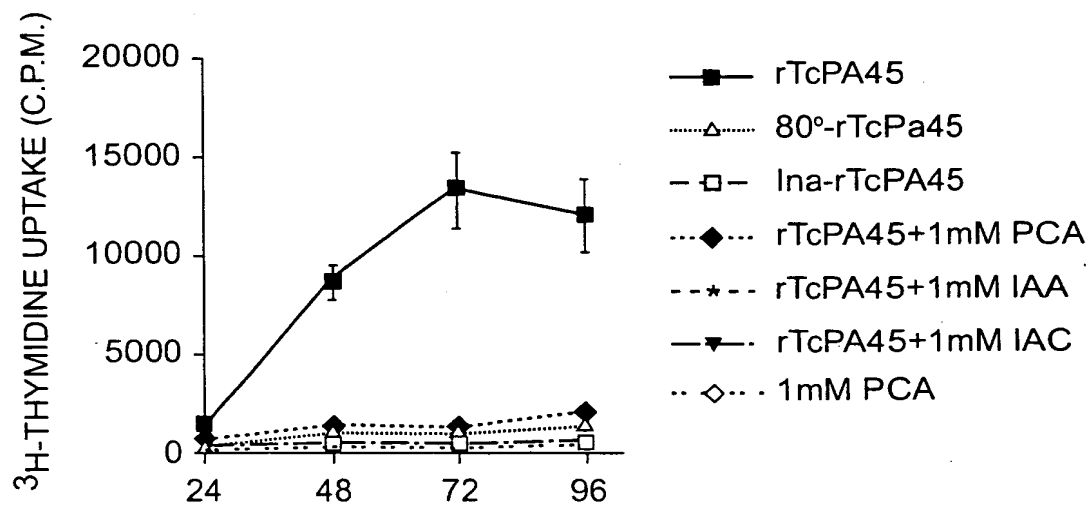


FIG. 11A

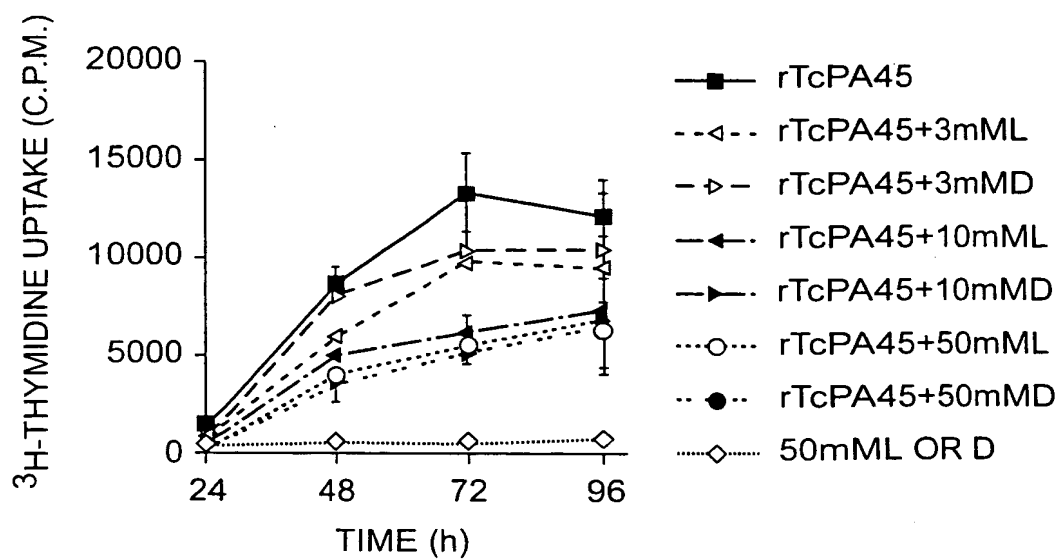


FIG. 11B

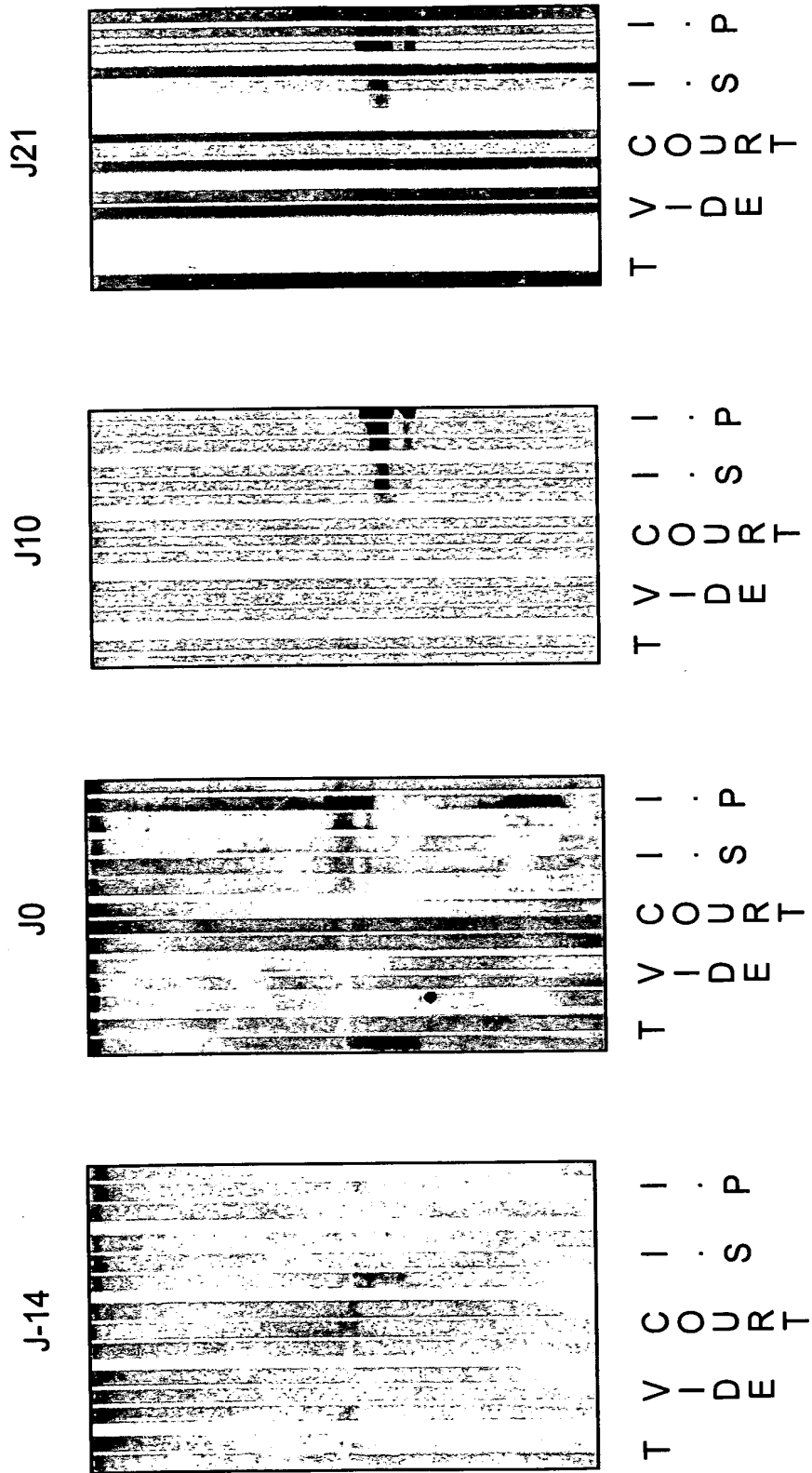


FIG. 12

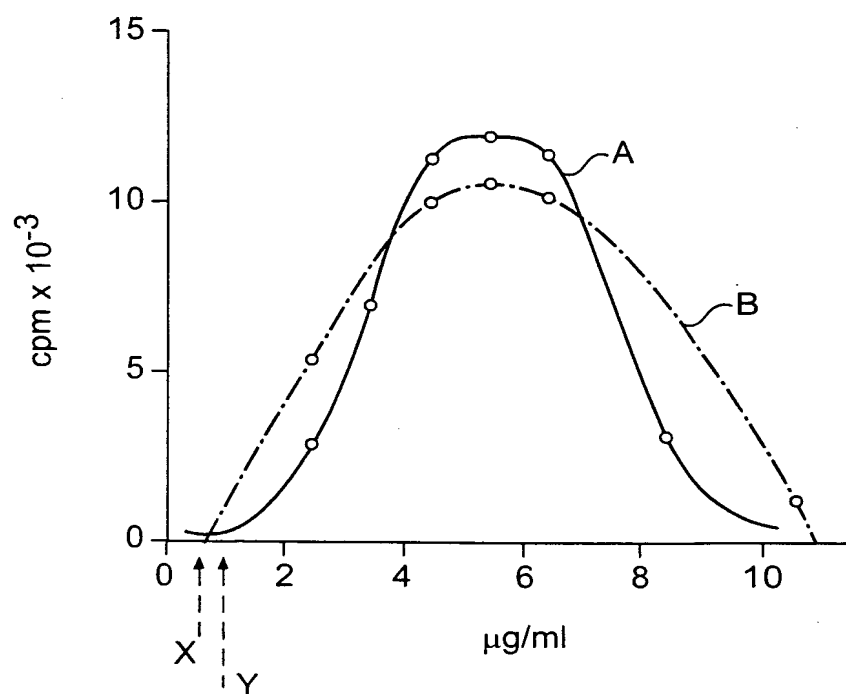


FIG. 13

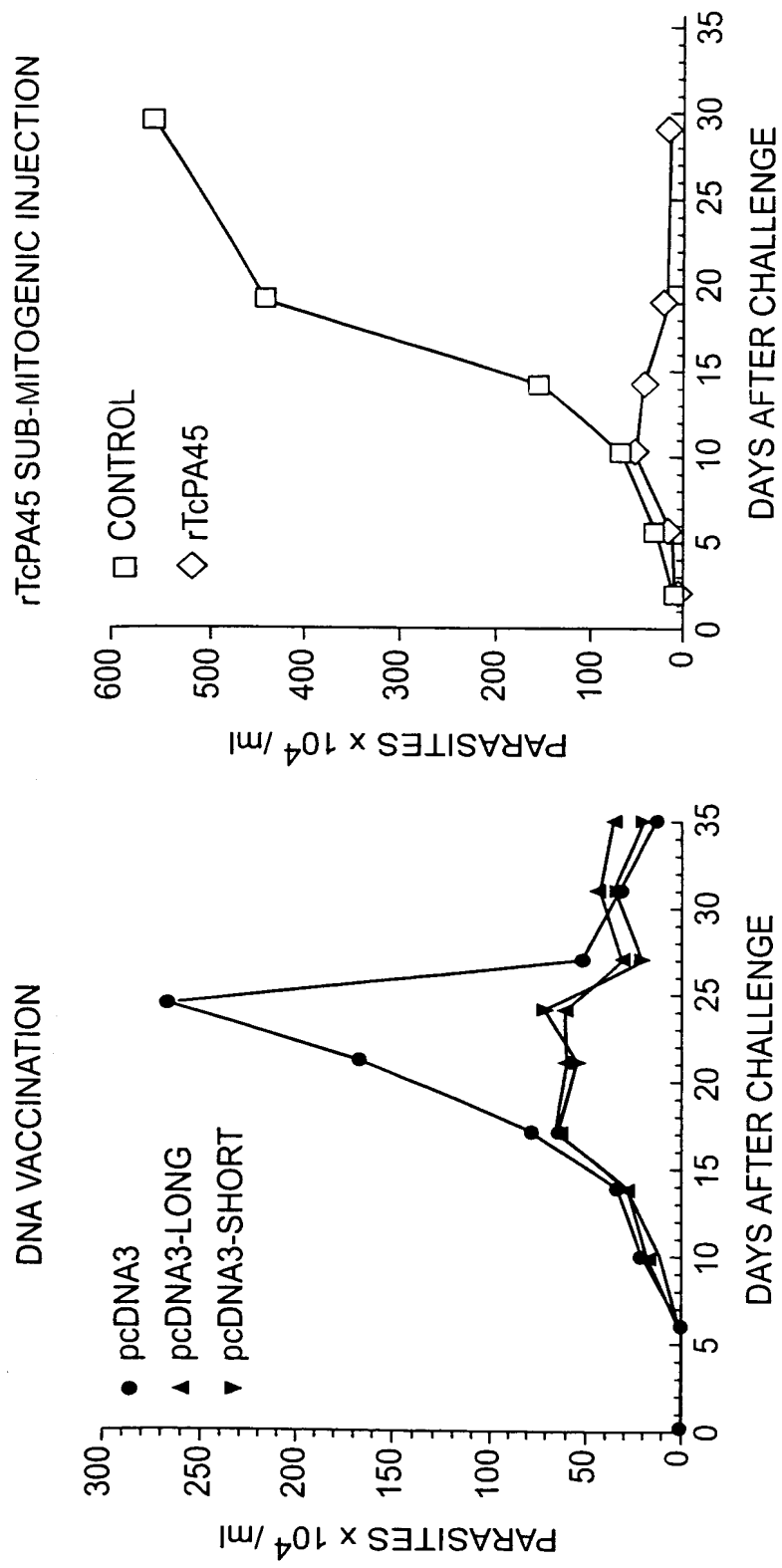


FIG. 14A

FIG. 14B

SEQ ID NO:2

Tc	RTGQEKLLFDQKYKLIKGEKKKKKNQRANRREHQQKREIMRFKKS	75
Tc	FTCIDMHTEGEAARIVTSGLPHPGSGNMAEKKAYLQENMDYLRRGIMLEPRGHDDMFGAFLFDPIEEGADLGMVF	150
Tc	MDTGGYLNMCCHNSIAAVTAAVETGIVSVPAKATNVPVVLDTPAGLVRGTAHLQSGTESEVSNASIIINVPSFLYQ	225
Tc	QDVVVVLPKPYGEVRVDIAFGGNFFAIVPAEQIGIDISVQNL SRLQEAGELLRTEINRSVKVQHPQLPHINTVDC	300
Tc	VEIYGPPTNPEANYKMVVIFGNRQADR SPCGT GTSAKMATLYAKGQLRIGETFVYESILGSLFQGRV--LGEE	371
Tc	RIPGVKVPVTKDAEEGMLVVTAEITGKAFIGFNTMLFDPTDPFKNGFTLKQ* 423	

FIG. 15

SEQ ID NO:4

Tc		MRFKKS	75
Tc	FTCIDMHTEGEAA <u>RI</u> VTSGLP <u>HI</u> PGSNMAEKKAYLQENMDYLRRGIMLEPRGHDDMFGAFLFDPIEEGADLGVMF		150
Tc	MDTGGYLNMCCHNSIAAVTAAVETGIVSVPAKATNVPVVDTPAGLVRGTAHLQSGTESEVSNASIIINVPSFLYQ		225
Tc	QDVVVLPKPYGEVRVDIAFGGNFFAIVPAEQLGIDISVQNLSRLQEAAGELLRTEINRSVKVQHPQLPHINTVDC		300
Tc	VEIYGPPTNPEANYK <u>NV</u> IFGNRQADR	SPCGT	371
Tc	RIPGVKVPVTKDAEEGMLVVVTAEITGKAFIMGFNTMLFDPTDPFKNGFTLKQ*		423

FIG. 16

SEQ ID NO:7

POLYPYRIMIDINE RICH REGION



SPLICE LEADER
ACCEPTOR SITES

SIGNAL PEPTIDE

CCTTTTCTTTTAAAAACAAAAATTCGGGGGGAATATGGAACAGGGTATATCGGTAAAGTGCTGTCCCAACAAAAATTTT 90
M R K S V C P K Q K F F 12
TTTTCCGCCCTCCCATTTTTTTTTTTTGTGTGTTCCCTTGATCTCTCGAACAGGCAGGAAAAGCTTCTGTTCACCAAAAAATAT 180
F S A F P F F F F C V F P L I S R T G Q E K L L F D Q K Y 42
AAATTTAAGGGCGAGAAAAAGAAAAATCAACGAGCAACAGGAGAGAACCAACAAAAAGGAAATTTATCGGATTT 270
K I I K G E K K E K K N Q R A N R R E K Q Q K R E I M R F 72
AAGAAATCATTACATCGACATGCATACGGAAGGTGAACGACGCGGATTGTGACGAGTGGTTGCCACACATTCAGGTTCGAAT 360
K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N 102
ATGGCGGAGAAAGCATACCTGCAGGAAAAACATGGATTATTGAGGCGTGGCATAATGCTGGAACCCACGTGGTCATGATGATATGTTT 430
M A E K K A Y L Q E N M D Y L R R G I M L E P R G K D D M F 132
GGAGCCTTTTATTGACCTATTGAAGAAGCGCTGACTTGGGCAATGGTATTCATGGATACCGGTGGCTATTTAAATATGTGTGGACAT 520
G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G H 162
AACTCAATTGCAGCGGTACGGCGGCAGTTGAAACGGGAATTGTGAGCGTGCCGCGAAGGCAACAAATGTTCCGGTTGTCTCTGGACACA 610
N S I A A V T A A V E T G I V S V P A K A T N V P V L D T I 192
CCTGCGGGGTGGTCCCGGTACGGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAATGCGAGTATTATCAATGATACCCCTCATTT 700
P A G L V R G T A R L Q S G T E S E V S N A S I I N V P S F 222
TTGTATCAGCAGGATGTGTGTTGTGTGCCAAAGCCCTATGTTGAAGTACGGGTGATATTGCATTGGAGGCAATTTTTCGCCCAT 790
L Y Q Q D V V V V L P K P Y G E V R V D I A F G G N F F A I 252

FIG. 17A

GTTCCTCCGGAGCAGTTGGGAATTGATAATCTCCGTTCAAAACCTCTCCAGGCTGCAGGAGGCAGGAACTTCTGCGTACTGAAATCAAT 880
V P A E Q L G I D I S V Q N L S R L Q E A G E L L R T E I N 282
CGCAGTGTGAAGTTTCAGCACCCCTCAGCTGCCCCATATTAAACACTGTGGACTGTGTGAGATATACGCTCCGCCCAACGAACCCGGAGGCA 970
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A 312
AACTACAAGAACGTTGTGATATTGGCAATCGCCAGGGGATCGCTCTCCATGTGGACAGGCACCAGCGCCCAAGATGGCAACACTTTAT 1060
N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y 342
GCCAAAGGCCAGCTTCGCATCGGAGAGACTTTTGTACGAGAGCATACTCGGCTCACTCTCCAGGCGAGGTACTTGGGAGGAGCGCA 1150
A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 372
ATACCGGGGTGAAGTGCCGGTGACCAAAAGATCCGAGGAAGGATGCTCGTTGTAACGGCAGAAATTACTGGAAGGCTTTTATCATG 1240
I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 402
GGTTTCAACACCATGCTGTTGACCCCAACGGATCCGTTTAAGAACGGATTTCACATTAAAGCAGTAGATCTGGTAGAGCACAGAAACTATT 1330
G F N T M L F D P T D P F K N G F T L K Q * 423
GGGGAACACGTGCGAACAGGTGCTGCTACGTGAAGGTATTGAATCGTTTTTTTTTTTATTATTTTATTATTATTATTAGTGCATT 1420

ATTATTAAATTTTTTTTTTGGGGTTTCAACGGTACCGGTTGGGAGCAGGGAAGCGATAGCGCGCGGACAAATTTTTTGTCTTTAT 1510

TTTTCATTTTCATCTTCCACCCCAACCCCTTGGTTCCACCGGTCCGCGGGGGTCTTGTGGGTGAGGAGTCCCTAAATCCCGCACCTCGG 1600

AGGAATAAACATATTTCAAATTTCATATCTTGGAAATCAAAAGGCAT 1651

POLYADENILATION SITE

Obs: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS
FOR CLONING

(b) NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

FIG. 17B

SEQ ID NO:8

ATGCGTAAAGTGTCTGTCTCCCAACAAAAATTTT 90
M R K S V C P K Q K F F 12
TTTTCGCGCTTCCCATTTTTTTTTTTTTTTTTTTT 180
F S A F F F F F F C V F P L I S R T G Q E K L L F D Q K Y 42
AAATTTAAGGCGAGAAAAAAGAAAAATCAACGAGCAACACGAGAGAACCAACAAAAAGGAAATTTATCGGATTT 270
K I I K G E K K E K K N Q R A N R R E H Q Q K R E I M R F 72
AAGAAATCATTCACATGCATCGACATCGAATCGGAAGGTGAAGCAGCAGGATTGTGACGAGTGGTTGCCACACATTCAGGTTCGAAT 360
K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N 102
ATGGCGGAGAAAGCATACCTGCAGGAAACATGGATTATTTGAGCGTGGCATAATGCTGGAACCCACGTGGTCATGATATGTTT 430
M A E K K A Y L Q E N M D Y L R R G I M L E P R G H D D M F 132
GGAGCCTTTTATTGACCCCTATTGAAGAAGGCGTGACTTGGGCATGGTATTCATGGATACCGTGGCTATTTAAATATGTGTGGACAT 520
G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G H 162
AACTCAATTGCAGCGGTTACGCGCGAGTTGAAACGGGAATTGTGAGCGTGCCGCGAAGGCAACAAATGTTCCGGTTGTCTCTGGACACA 610
N S I A A V T A A V E T G I V S V P A K A T N V P V L D T 192
CCTGCGGGGTTGGTGC GCGGTACGGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAATCGGAGTATTATCAATGTACCCTCATTT 700
P A G L V R G T A H L Q S G T E S E V S N A S I I N V P S F 222
TTGTATCAGCAGGATGTGGTGTGTGTTGCCAAAGCCCTATGGTGAAGTACGGGTTGATATTGCCATTTGGAGGCAATTTTTCGCCCAT 790
L Y Q Q D V V V V L P K P Y G E V R V D I A F G G N F A I 252
GTTCCCGGAGCAGTTGGGAATTGATATCTCCGTTCAAACCTCTCCAGGTCGAGGAGCAGGAGAACTTCTGCGTACTGAAATCAAT 880
V P A E Q L G I D I S V Q N L S R L Q E A G E L L R T E I N 282
CGCAGTGTGAAGGTTCAGCACCCCTCAGCTGCCCCATATTAACTGTGGACTGTGTGAGATATACGGTCCGCCAACGAACCCGGAGGCA 970
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A 312

FIG. 18A

AACTACAAGAACGGTGTGATATTTGGCAATCGCCAGGGGATCGCTCTCCATGTGGACAGGCACCAGCGCCAAGATGGCAACACTTTAT 1060
N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y 342
GCCAAAGGCCAGCTTCGCATCGGAGAGACTTTTGTGTACGAGAGCATACTCGGCTCACTCTCCAGGGCAGGGTACTTGGGGAGGAGCGGA 1150
A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 372
ATACCGGGGGTGAAGGTCCCGGTGACCAAGATCCCGAGGAAGGATGCTCGTTGTAAACGGCAGAAATTACTGGAAGGCTTTTATCATG 1240
I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 402
GGTTTCAACACCATGCTGTTGACCCCAACGGATCCGTTTAAGAACGGATTACATTAAAGCAGTAGATCTGGTAGAGCACAGAAACTATT 1330
G F N T M L F D P T D P F K N G F T L K Q * 423
GGGAACACGTGCGAACAGGTGCTGCTACGTGAAGGTATTGAATGAATCGTTTTTTTATTTTATTTTATTTTATTTATTTATTTAGTGCAAT 1420

ATTATTAAATTTTTTTTTTGGGTTTCAACGGTACCGCGTTGGAGCAGGGAAGCATAGCGGCCGGACAAATTTTTTGCTTTTAT 1510

TTTTCATTTTCATCTTCCTACCCCAACCCCTTGGTTCCACCGTCCGGCGGGGTCTTGTGGTGGAGGAGTCTCTAAATCCCCGACCTCGG 1600

AGGAATAAACATATTTCAATTTTCATATCTTGGAAATCAAAAGGCAT 1651

POLYADENILATION SITE

Obs: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS
FOR CLONING

NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

FIG. 18B

SEQ ID NO:9

CGAACAGGGCAGGAAAAGCTTCTGTGTGACCAAAATAT 270
R T G Q E K L L F D Q K Y 72
AAAATTATTAGGGCGAGAAAAGAAAATCAACGAGCAACAGGAGAACACCAAAAAGGAAATATTATGCGATTT 360
K I I K G E K K E K K N Q R A N R R E H Q Q K R E I M R F 102
AAGAAATCATTCACATCGACATGCATACGGAAGGTGAACGAGCAGCGATTGTGACGAGTGGTTTGCCACACATTCAGGTTCGAAT 430
K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N 132
ATGGCGGAGAAAGCATACCTGCAGGAAAACATGGATTATTGAGGCGTGGCATAATCTGGAACCCACGTGGTCATGATGATATGTTT 520
M A E K K A Y L Q E N M D Y L R R G I M L E P R G H D D M F 162
GGAGCCTTTATTGACCCATTGAAGAAGCGCTGACTTGGGCATGGTATTTCATGGATACCGGTGGCTATTTAAATATGTGTGGACAT 610
G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G H 192
AACTCAATTGCAGCGGTTACGGCGGAGTTGAAACGGGAATTGTAGCGTGCCGCGAAGGCAACAATGTTCCGGTTGTCTCTGGACACA 700
N S I A A V T A A V E T G I V S V P A K A T N V P V L D T 222
CCTGCGGGGTTGGTCCGGGTACGGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAATCGGAGTATTATCAATGTACCCTCATT 790
P A G L V R G T A H L Q S G T E S E V S N A S I I N V P S F 252
TTGTATCAGCAGGATGTGGTGGTTGTGTGCCAAAGCCCTATGGTGAAGTACGGGTTGATATTGCCATTTGGAGGCCAATTTTTCGCCCAT 880
L Y Q Q D V V V V L P K P Y G E V R V D I A F G G N F A I 282
GTTCCCGCGGAGCAGTTGGGAATTGATATCTCCGTTCAAACCTCTCCAGGCTGCAGGAGGAGGAGAACTTCTGCGTACTGAAATCAAT 970
V P A E Q L G I D I S V Q N L S R L Q E A G E L L R T E I N 312
CGCAGTGTGAAGGTTACGACCCCTCAGCTGCCCATATTAAACACTGTGGACTGTGTGAGATATACGGTCCGCCAACGAACCCGAGGCA 1060
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A 342
AACTACAAGAACGTTGTGATATTGGCAATCGCCAGCGCGATCGCTCTCCATGTGGGACAGGCACCGCCCAAGATGGCAACACTTTAT 1150
N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y 372

FIG. 19A

GCCAAAGGCCAGCTTCGCATCGGAGAGACTTTTGTGTACGAGAGCATACTCGGCTCACTCTTCCAGGGCAGGGTACTTGGGGAGGAGCGA 1240
A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 402
ATACCGGGGGTGAAGGTGCCCGTGACCAAAAGATGCCGAGGAAGGATGCTCGTTGTAACGGCAGAAAATTACTGGAAGGCTTTTATCATG 1330
I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 423
GGTTTCAACACCATGCTGTTTGACCCCAACGGATCCGTTTAAGAACGGATTTCACATTAAAGCAGTAGATCTGGTAGAGCACAGAAACTATT 1420
G F N T M L F D P T D P F K N G F T L K Q *
GGGGAACACGTGCGAACAGGTGCTGCTACGTGAAGGTATTGAATGAATCGTTTTTTTATTTTATTTTATTTTATTTATTTAGTGCAAT 1510

ATTATTAAATTTTTTTTTTGGGGTTTCAACGGTACCGGTTGGGAGCAGGAAGCGATAGCGGCCGACAAATTTTTTGCTTTTAT 1600

TTTTCATTTTCATCTTCCTACCCAAACCCCTTGGTTCCACCGGTCGCGGGGGGTCTTGTGGGTGAGAGTCCTAAATCCCGCACCTCGG 1651

AGGAATAAACATATTTCAAATTCATATCTTGGAATCAAAAGGCAT

POLYADENILATION SITE

Obs: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS
FOR CLONING

NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

FIG. 19B

SEQ ID NO:10

SIGNAL PEPTIDE

ATGCCGTAAAGTGTCGTGCCCAACAAATTTT

TTTTCCGCCCTTCCCATTTTTTTTTTTTGTGTGTTCCCTTGATCTCT

NUCLEOTIDE SEQUENCE OF SIGNAL SEQUENCE TcPA45

FIG. 20

SEQ ID NO:11

ATGCGATTT 360
M R F 102
AAGAAATCATTACATGCGATCGACATGCATACGGAAGGTGAAGCAGCAGCGGATTGTGACGAGTGGTTGCCACACATTCAGGTTCCAAT 430
K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N 132
ATGGCGGAGAGAAAGCATACCTGCAGGAAAACATGGATTATTTCAGGCGTGGCATAATGCTGGAACCCACGTTGGTCATGATATGTTT 520
M A E K K A Y L Q E N M D Y L R R G I M L E P R G H D M F 162
GGAGCCTTTTATTGACCCCTATTGAAGAAGCGCTGACTTGGGCATGGTATTTCATGGATACCGGTGGCTATTTAAATATGTGTGGACAT 610
G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G H 192
AACTCAATTGCAGCGGTTACGGCGGAGTTGAAACGGGAATTGTGAGCGTGCCGGGAAGCAACAATGTTCCGGTTGTCTGGACACA 700
N S I A A V T A A V E T G I V S V P A K A T N V P V L D T 222
CCTGCGGGGTTGGTGGCGGTACGGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAAATGCGAGTATTATCAATGTACCCCTCATTT 790
P A G L V R G T A H L Q S G T E S E V S N A S I I N V P S F 252
TTGTATCAGCAGGATGGTGGTTGTGTTGCCAAAGCCCTATGGTGAAGTACGGGTGATATTGCAATTTGGAGGCAATTTTTCGCCCAT 880
L Y Q Q D V V V L P K P Y G E V R V D I A F G G N F A I 282
GTTCCCGGAGCAGTTGGGAATTGATATCTCCGTTCAAACCTCTCCAGGCTGCAGGAGGCGAGGAGAACTTCTGCGTACTGAAATCAAT 970
V P A E Q L G I D I S V Q N L S R L Q E A G E L L R T E I N 312
CGCAGTGTGAAGGTTCAGCACCCCTCAGCTGCCCATATTAAACACTGTGGACTGTGTTGAGATATACGGTCCGCCAACGAACCCGGAGGCA 1060
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A 342
AACTACAAGAAGTTGTGATATTGGCAATCGCCAGGCGGATCGCTCTCCATGTGGACAGGCACCAGCGCCAAGATGGCAACACTTTAT 1150
N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y 372
GCCAAAGCCAGCTTCGCATCGGAGAGACTTTTGTGTACGAGAGCATACTCGGCTCACTCTTCCAGGGCAGGTACTTGGGAGGAGCGA 1240
A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 402

FIG. 21A

ATACCGGGGTGAAGTGCCGGTGACCAAGAATGCCGAGGAAGGATGCTCGTTGTAAAGGCAGAAATTACTGGAAGGCTTTTATCATG 1330
I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 423
GGTTCAACACCATGCTGTTTGACCCCAACGGATCCGTTTAAACAACGGATTACACATTAAAGCAGTAGATCTGGTAGAGCACAGAAACTATT 1420
G F N T M L F D P T D P F K N G F T L K Q *
GGGGAACACGTGCGAACACAGGTGCTGCTACGTGAAGGTATTGAATGAATCGTTTTTTTTTATTATTTTATTATTTATTTAGTGCATT 1510
ATTATTAAATTTTTTTTTTTTGGGGTTTCAACGGTACCGCGTTGGGAGCAGGGAAGCGATAGCGGCCGGACAATTTTTTGGCTTTTAT 1600
TTTCATTTTCACTTCCTACCCAAACCCCTTGGTTCCACCGGTCCGGCGGGGGTCTTGTGGGTGGAGAGTCCTAAATCCCGCACCTCGG 1651
AGGAATAAACATATTCAATTCATATCTTGGAATCAAAAGGCAT

FIG. 21B